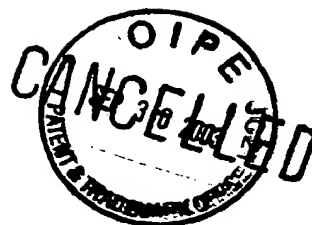




02480 U.S. PTO

SEQUENCE LISTING



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<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009070US

<140> US 09/886,349

<141> 2001-06-20

<150> US 09/597,796

<151> 2000-06-20

<150> US 60/265,737

<151> 2001-02-01

<160> 50

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> MTB32A (Ra35FL)

<220>

<221> modified_base

<222> (1)..(1872)

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 tacggtgact attacgtgtg gagcgacacc agcgagcgct acaccgacgc ccggatcatc 1800
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 <211> 355
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB32A (Ra35FL)

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 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220

Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240

Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320

Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350

Pro Pro Ala
 355

<210> 3
 <211> 1002
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB32A (Ra35 mature)

<400> 3
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 aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccg catcgatc 180
 gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
 gcgttcagcg tcggctccgg ccaaactac ggcgtcgatg tggtcgggta tgaccgcacc 300
 caggatgtcg cgggtgctgca gctgcgcggt gccgggtggc tgcgctcggc ggcgatcggt 360
 ggcggcgctc cgggttggtga gcccgctcgtc gcgatgggca acagcgggtg gcagggcgga 420
 acgccccgtg cgggtgcctgg cagggtgggc gcgctcggcc aaaccgtgca ggcgtcggat 480
 tcgctgaccg gtgccgaaga gacattgaac ggggtgatcc agttcgatgc cgcgatccag 540
 cccgggtgagg cgggcggggc cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg 600
 gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
 caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcaccac cgttcataat 720
 gggcctaccg ccttcctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
 caacgcgtgg tcgggagcgc tccggcgga agtctcggca tctccaccgg cgacgtgatc 840
 accgcggctc acggcgctcc gatcaactcg gccaccgca tggcggacgc gcttaacggg 900
 catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcgggagg caccggtaca 960
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<210> 4
 <211> 330
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>

<223> MTB32A (Ra35 mature)

<400> 4

Met	His	His	His	His	His	His	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	
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Phe	Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	
		20						25					30			
Gln	Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	
		35					40					45				
Asn	Ala	Val	Gly	Ala	Gly	Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	
	50					55					60					
Val	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	
	65				70					75					80	
Phe	Ser	Val	Gly	Ser	Gly	Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	
				85					90					95		
Asp	Arg	Thr	Gln	Asp	Val	Ala	Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	
			100					105					110			
Leu	Pro	Ser	Ala	Ala	Ile	Gly	Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	
		115					120					125				
Val	Ala	Met	Gly	Asn	Ser	Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	
	130					135					140					
Pro	Gly	Arg	Val	Val	Ala	Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	
	145				150					155					160	
Leu	Thr	Gly	Ala	Glu	Glu	Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	
			165					170						175		
Ala	Ile	Gln	Pro	Gly	Asp	Ser	Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	
			180					185					190			
Gln	Val	Val	Gly	Met	Asn	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	
		195					200					205				
Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	
	210					215					220					
Ala	Gly	Gln	Ile	Arg	Ser	Gly	Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	
	225				230					235					240	
Pro	Thr	Ala	Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	
			245					250						255		
Ala	Arg	Val	Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	
			260				265						270			
Ile	Ser	Thr	Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	
		275					280					285				
Ser	Ala	Thr	Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	
	290					295					300					

Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330

<210> 5
 <211> 1002
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra35FLMutSA

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 ttccccgcgc tgccccctcga cccgtccgcg atggtcgccc aagtggggcc acagggtggtc 120
 aacatcaaca ccaaaactggg ctacaacaac gccgtgggag ccgggaccgg catcgatcatc 180
 gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
 gcgttcagcg tcgggtccgg ccaaactac ggcgtcgatg tggtcgggta tgaccgcacc 300
 caggatgtcg cgggtgctga gctgcgcggt gccgggtggc tgccgtcggc ggcgatcggg 360
 ggccggcgctg cgggttggtga gcccgtcgtc gcgatgggca acagcgggtg gcagggcgga 420
 acgccccgtg cgggtgcctg cagggtgggtc gcgctcggcc aaaccgtgca ggcgtcggat 480
 tcgctgaccg gtgccgaaga gacattgaac ggggtgatcc agttcgatgc cgcgatccag 540
 cccgggtgatg cgggcggggc cgtcgtcaac ggcctaggac aggtgggtcgg tatgaacacg 600
 gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
 caggcgatgg cgatcgcggg ccagatccga tcgggtgggg gggtcaccac cgttcataatc 720
 gggcctaccg ccttcctcgg cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc 780
 caacgcgtgg tcgggagcgc tccggcgga agtctcggca tctccaccgg cgacgtgatc 840
 accgcgggtc acggcgctcc gatcaactcg gccaccgga tggcggacgc gcttaacggg 900
 catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcgggcgg cacgcgtaca 960
 gggaacgtga cattggccga gggacccccg gcctgagaat tc 1002

<210> 6
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra35FLMutSA

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 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
 20 25 30
 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
 35 40 45
 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
 50 55 60
 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65 70 75 80
 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
 85 90 95

Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 100 105 110
 Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
 115 120 125
 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 130 135 140
 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 145 150 155 160
 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 165 170 175
 Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
 180 185 190
 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 195 200 205
 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 210 215 220
 Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
 225 230 235 240
 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
 245 250 255
 Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330

<210> 7

<211> 585

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 7

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 tccgcgatgg tcgcccaggt ggggccacag gtggtcaaca tcaacaccaa actggggtac 120
 aacaacgccc tgggcgccgg gaccggcatc gtcatcgatc ccaacgggtg cgtgctgacc 180
 aacaaccacg tgatcgcggg cgccaccgac atcaatgcgt tcagcgctcg ctccggccaa 240
 acctacggcg tcgatgtggt cgggtatgac cgcaccacag atgtcgcggt gctgcagctg 300
 cgcggtgccg gtggcctgcc gtcggcggcg atcggtggcg gcgtcgcggt tggtagagcc 360

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gtcgtcgcga tgggcaacag cgggtgggcag ggcggaacgc cccgtgcggt gcctggcagg 420
gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480
ttgaacgggt tgatccagtt cgatgccgcg atccagcccg gtgaggcggg cgggcccgtc 540
gtcaacggcc taggacaggt ggtcggtatg aacacggccg cgtcc 585

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<210> 8
<211> 195
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> Ra35 N-terminus of MTB32A (Ra35FL)

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Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
      20             25             30

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
      35             40             45

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
      50             55             60

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
      65             70             75             80

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
      85             90             95

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
      100            105            110

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
      115            120            125

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
      130            135            140

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
      145            150            155            160

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
      165            170            175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
      180            185            190

Ala Ala Ser
      195

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<210> 9
<211> 447
<212> DNA
<213> Mycobacterium tuberculosis

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<220>

<223> Ra12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 9

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caccgttcat atcgggccta ccgccttctt cggcttgggt gttgtcgaca acaacggcaa 180
cggcgacacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcattctccac 240
cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300
cgcgcttaac gggcatcatc ccggtgacgt catctcgggt aactggcaaa ccaagtcggg 360
cggcacgcgt acagggaacg tgacattggc cgagggaccc ccggcctgat ttcgtcgygg 420
ataccaccgc ccggccggcc aattgga 447
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<210> 10

<211> 132

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> Ra 12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 10

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Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
  1             5             10             15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
      20             25             30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
  35             40             45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
  50             55             60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
  65             70             75             80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85             90             95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
      100            105            110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
      115            120            125

Gly Pro Pro Ala
      130
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<210> 11

<211> 851

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> MTB39 (TbH9)

<220>
 <221> modified_base
 <222> (767)
 <223> n = g, a, c or t

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 ccgggttgct gcggcggcct acgagacggc gtatgggctg acggtgcccc cgccgggtgat 120
 cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180
 cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccagg acgccgccgc 240
 gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
 ggcgcgggag atgaccagcg cgggtgggct cctcgagcag gccgccgcgg tcgaggaggc 360
 ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccaggcgc tgaaacagtt 420
 ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
 ctgcgccgat cggtcgccga tcagcaacat ggtgtcgatg gccacaacc acatgtcgat 540
 gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600
 ggcggcggcc gccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
 gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
 ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcanagt ctggtcggcg 780
 gaacggtggt ccggcgtaag gtttaccccc gttttctgga tgcggtgaac ttcgtcaacg 840
 gaaacagtta c 851

<210> 12
 <211> 263
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB39 (TbH9)
 <220>
 <221> MOD_RES
 <222> (254)
 <223> Xaa = any amino acid

<400> 12
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 Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20 25 30
 Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35 40 45
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50 55 60
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110
 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
 115 120 125

Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
 130 135 140
 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 145 150 155 160
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 165 170 175
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 180 185 190
 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
 195 200 205
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220
 Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255
 Arg Arg Asn Gly Gly Pro Ala
 260

<210> 13
 <211> 3058
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB39 (TbH9FL)

<400> 13
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 ggcataccca gagatgttgg cggcggcgcc tgacaccctg cagagcatcg gtgctaccac 120
 tgtggctagc aatgccgctg cggcggcgcc gacgactggg gtggtgcccc ccgctgccga 180
 tgaggtgtcg gcgctgactg cggcgcaact cgccgcacat gcggcgatgt atcagtccgt 240
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 tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
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 aggaggcgcc ggagatgacc agcgcgggtg ggctcctcga gcaggccgcc gcggtcgagg 960
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 <213> Mycobacterium tuberculosis

<220>
 <223> MTB39 (TbH9FL)

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 35 40 45
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	130	135	140
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	145	150	155
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	165	170	175
Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	180	185	190
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	195	200	205
Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	210	215	220
Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	225	230	235
Met	Val	Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	245	250	255
Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	260	265	270
Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	275	280	285
Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	290	295	300
Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	305	310	315
Pro	Gln	Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	325	330	335
Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	340	345	350
Gln	Met	Leu	Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	355	360	365
Gly	Gly	Leu	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	370	375	380
Pro	His	Ser	Pro	Ala	Ala	Gly										385	390	

<210> 15

<211> 2287

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: tri-fusion protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 fusion)

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 <222> (42)..(2231)
 <223> MTB72F

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 <222> (30)
 <223> n = g, a, c or t

<220>
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 <222> (33)
 <223> n = g, a, c or t

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 <223> n = g, a, c or t

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 His His Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln
 10 15 20

gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc 152
 Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 25 30 35

cga tcg ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc 200
 Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe
 40 45 50

ctc ggc ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa 248
 Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln
 55 60 65

cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc 296
 Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly
 70 75 80 85

gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg 344
 Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala
 90 95 100

atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg 392
 Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val
 105 110 115

acc tgg caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg 440
 Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu
 120 125 130

gcc gag gga ccc ccg gcc gaa ttc atg gtg gat ttc ggg gcg tta cca 488
 Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro
 135 140 145

ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg	536
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser	
150 155 160 165	
ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt	584
Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe	
170 175 180	
tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg	632
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly	
185 190 195	
tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg	680
Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro	
200 205 210	
tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc	728
Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala	
215 220 225	
gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg	776
Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	
230 235 240 245	
acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att	824
Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	
250 255 260	
ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc	872
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	
265 270 275	
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg	920
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met	
280 285 290	
ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg	968
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro	
295 300 305	
ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag	1016
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln	
310 315 320 325	
gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg	1064
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu	
330 335 340	
atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag	1112
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln	
345 350 355	
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg	1160
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser	
360 365 370	
ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac	1208
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His	
375 380 385	

atg	tcg	atg	acc	aac	tcg	ggg	gtg	tcg	atg	acc	aac	acc	ttg	agc	tcg	1256
Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	
390					395					400					405	
atg	ttg	aag	ggc	ttt	gct	ccg	gcg	gcg	gcc	cgc	cag	gcc	gtg	caa	acc	1304
Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Arg	Gln	Ala	Val	Gln	Thr	
			410						415					420		
gcg	gcg	caa	aac	ggg	gtc	cgg	gcg	atg	agc	tcg	ctg	ggc	agc	tcg	ctg	1352
Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu	
			425					430					435			
ggg	tct	tcg	ggg	ctg	ggc	ggg	ggg	gtg	gcc	gcc	aac	ttg	ggg	cgg	gcg	1400
Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	
		440					445					450				
gcc	tcg	gtc	ggg	tcg	ttg	tcg	gtg	ccg	cag	gcc	tgg	gcc	gcg	gcc	aac	1448
Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala	Trp	Ala	Ala	Ala	Asn	
	455					460					465					
cag	gca	gtc	acc	ccg	gcg	gcg	cgg	gcg	ctg	ccg	ctg	acc	agc	ctg	acc	1496
Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	
470					475					480					485	
agc	gcc	gcg	gaa	aga	ggg	ccc	ggg	cag	atg	ctg	ggc	ggg	ctg	ccg	gtg	1544
Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu	Gly	Gly	Leu	Pro	Val	
			490					495						500		
ggg	cag	atg	ggc	gcc	agg	gcc	ggg	ggg	ctc	agt	ggg	gtg	ctg	cgt		1592
Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Leu	Ser	Gly	Val	Leu	Arg		
			505				510					515				
gtt	ccg	ccg	cga	ccc	tat	gtg	atg	ccg	cat	tct	ccg	gca	gcc	ggc	gat	1640
Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser	Pro	Ala	Ala	Gly	Asp	
		520					525					530				
atc	gcc	ccg	ccg	gcc	ttg	tcg	cag	gac	cgg	ttc	gcc	gac	ttc	ccc	gcg	1688
Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	
	535					540					545					
ctg	ccc	ctc	gac	ccg	tcc	gcg	atg	gtc	gcc	caa	gtg	ggg	cca	cag	gtg	1736
Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Gly	Pro	Gln	Val	
550					555					560					565	
gtc	aac	atc	aac	acc	aaa	ctg	ggc	tac	aac	aac	gcc	gtg	ggc	gcc	ggg	1784
Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	
			570					575						580		
acc	ggc	atc	gtc	atc	gat	ccc	aac	ggg	gtc	gtg	ctg	acc	aac	aac	cac	1832
Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	
			585					590					595			
gtg	atc	gcg	ggc	gcc	acc	gac	atc	aac	gcg	ttc	agc	gtc	ggc	tcc	ggc	1880
Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	
		600					605					610				
caa	acc	tac	ggc	gtc	gat	gtg	gtc	ggg	tat	gac	cgc	acc	cag	gat	gtc	1928
Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	
	615					620					625					

gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc	1976
Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
630 635 640 645	
ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	2024
Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
650 655 660	
ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	2072
Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
665 670 675	
ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag	2120
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
680 685 690	
aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	2168
Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
695 700 705	
tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	2216
Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
710 715 720 725	
acg gcc gcg tcc tag gatatccatc acactggcgg ccgctcgagc agatccggt	2271
Thr Ala Ala Ser	
730	
gtaacaaagc ccgaaa	2287

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<211> 729

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:tri-fusion
protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39
fusion)

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Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30

Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
35 40 45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95

Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110

Asp	Val	Ile	Ser	Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	115	120	125
Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Met	Val	Asp	130	135	140
Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly	145	150	155
Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val	165	170	175
Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp	180	185	190
Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	195	200	205
Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	210	215	220
Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	225	230	235
Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	245	250	255
Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	260	265	270
Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	275	280	285
Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	290	295	300
Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	305	310	315
Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	325	330	335
Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu	340	345	350
Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	355	360	365
Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	370	375	380
Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	385	390	395
Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Arg	405	410	415
Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	420	425	430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 17
 <211> 2190
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MTB72FMutSA
 (Ra12-TbHp-Ra35MutSA) cDNA

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<400> 17
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cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat ccgatcgggt 120
gggggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tgttgtcgac 180
aacaacggca acggcgcgacg agtccaacgc gtggctcgga gcgctccggc ggcaagtctc 240
ggcatctcca ccggcgacgt gatcacgcg gtcgacggcg ctccgatcaa ctcggccacc 300
gcgatggcgg acgcgcttaa cgggcatcat cccggtgacg tcatctcggt gacctggcaa 360
accaagtcgg gcggcacgcg tacagggaac gtgacattgg ccgagggacc cccggccgaa 420
ttcatgggtg atttcggggc gttaccaccg gagatcaact ccgcgaggat gtacgccggc 480
ccgggttcgg cctcgctggg ggccgcggct cagatgtggg acagcgtggc gagtgcctg 540
ttttcggccg cgtcggcggt tcagtcgggt gtctgggggtc tgacgggtggg gtcgtggata 600
ggttcgtcgg cgggtctgat ggtggcggcg gcctcgccgt atgtggcgtg gatgagcgtc 660
accgcggggc aggcgcgagc gaccgccgcc caggtcgggg ttgctgcggc ggcctacgag 720
acggcgtagt ggctgacggt gccccgcgcg gtgatcgccg agaaccgtgc tgaactgatg 780
attctgatag cgaccaacct cttggggcaa aacaccccg cgatcgcggt caacgaggcc 840
gaatacggcg agatgtgggc ccaagacgcc gccgcgatgt ttggctacgc cgcggcgacg 900
gcgacggcga cggcgacgtt gctgccgttc gaggaggcgc cggagatgac cagcgcggg 960
gggctcctcg agcaggccgc cgcggtcgag gaggcctccg acaccgccgc ggcgaaccag 1020
ttgatgaaca atgtgcccc aagcgtgcaa cagctggccc agcccacgca gggcaccacg 1080
ccttcttcca agctgggtgg cctgtggaag acggtctcgc cgcacgggtc gccgatcagc 1140
aacatgggtg cgatggccaa caaccacatg tcgatgacca actcgggtgt gtcgatgacc 1200
aacaccttga gctcgatgtt gaagggtttt gctcgggcgg cggccgcccc ggccgtgcaa 1260
accgcggcgc aaaacggggg ccgggcgatg agctcgctgg gcagctcgct gggttcttcg 1320
gggtctggcg gtgggggtgg ccgcaacttg ggtcgggcgg cctcggtcgg ttcgttgtcg 1380
gtgccgcagg cctgggccgc ggccaaccag gcagtcaccc cggcggcgcg ggcgtgccg 1440
ctgaccagcc tgaccagcgc cgcggaaaga gggcccgggc agatgctggg cgggctgccg 1500
gtggggcaga tgggcgccag ggccggtggt gggctcagtg gtgtgctgcg tgttcgccg 1560
cgacctatg tgatgccgca ttctccggca gccggcgata tcgccccgcc ggccttgtcg 1620
caggaccggt tcgccgactt cccgcgctg cccctcgacc cgtcccgcat ggtcgcccaa 1680
gtggggccac aggtggtcaa catcaacacc aaactgggct acaacaacgc cgtgggcgcc 1740
gggaccggca tcgtcatcga tcccaacggg gtcgtgctga ccaacaacca cgtgatcgcg 1800
ggcgccaccg acatcaatgc gttcagcgtc ggtccgggcc aaacctacgg cgtcgatgtg 1860
gtcgggtatg accgcaccca ggatgtcgcg gtgctgcagc tgcgcggtgc cgggtggcctg 1920
ccgtcggcgg cgatcggtgg cggcgtcgcg gttggtgagc ccgtcgtcgc gatgggcaac 1980
agcgggtggc agggcggaac gcccgtgcg gtgcctggca ggggtggtcg gctcggccaa 2040
accgtgcagg cgtcggattc gctgaccggt gccgaagaga cattgaacgg gttgatccag 2100
ttcgatgccg cgatccagcc cggatgatgc ggcggggccc tcgtcaacgg cctaggacag 2160
gtggtcggtg tgaacacggc cgcgtcctag 2190
```

<210> 18
 <211> 729
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MTB72FMutSA
 (Ra12-TbHp-Ra35MutSA)

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<400> 18
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
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Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220
 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300
 Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335

Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala
 405 410 415
 Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
660 665 670

Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
675 680 685

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
690 695 700

Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720

Val Val Gly Met Asn Thr Ala Ala Ser
725

<210> 19
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:bi-fusion
protein TbH9-Ra35 (designated MTB59F)

<220>
<221> CDS
<222> (1)..(1791)
<223> MTB59F

<400> 19
cat atg cat cac cat cac cat cac atg gtg gat ttc ggg gcg tta cca 48
His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
1 5 10 15

cgc gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg 96
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
20 25 30

ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt 144
Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
35 40 45

tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg 192
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
50 55 60

tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg 240
Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65 70 75 80

tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc 288
Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
85 90 95

gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg 336
Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
100 105 110

acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att	384
Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	
115 120 125	
ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc	432
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	
130 135 140	
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg	480
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met	
145 150 155 160	
ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg	528
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro	
165 170 175	
ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag	576
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln	
180 185 190	
gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg	624
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu	
195 200 205	
atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag	672
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln	
210 215 220	
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg	720
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser	
225 230 235 240	
ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac	768
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His	
245 250 255	
atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg	816
Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser	
260 265 270	
atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc gtc caa acc	864
Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr	
275 280 285	
gcg gcg caa aac ggg gtc ccg gcg atg agc tcg ctg ggc agc tcg ctg	912
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu	
290 295 300	
ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg	960
Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala	
305 310 315 320	
gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac	1008
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn	
325 330 335	
cag gca gtc acc ccg gcg gcg ccg gcg ctg ccg ctg acc agc ctg acc	1056
Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
340 345 350	

agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg	1104
Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
355 360 365	
ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt	1152
Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg	
370 375 380	
gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat	1200
Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
385 390 395 400	
atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc gcc gac ttc ccc gcg	1248
Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
405 410 415	
ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg	1296
Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
420 425 430	
gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1344
Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
435 440 445	
acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac	1392
Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
450 455 460	
gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1440
Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
465 470 475 480	
caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc	1488
Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
485 490 495	
gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc	1536
Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
500 505 510	
ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	1584
Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
515 520 525	
ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	1632
Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
530 535 540	
ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag	1680
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
545 550 555 560	
aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	1728
Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
565 570 575	
tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	1776
Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
580 585 590	

acg gcc gcg tcc tag gatatc
 Thr Ala Ala Ser
 595

1797

<210> 20
 <211> 596
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:bi-fusion
 protein TbH9-Ra35 (designated MTB59F)

<400> 20
 His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
 1 5 10 15
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60
 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65 70 75 80
 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95
 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110
 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
 115 120 125
 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
 145 150 155 160
 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
 165 170 175
 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
 180 185 190
 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
 195 200 205
 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
 210 215 220
 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
 245 250 255

Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	
			260						265					270		
Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	
		275					280					285				
Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu	
	290					295					300					
Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	
305					310					315					320	
Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala	Trp	Ala	Ala	Ala	Asn	
				325					330						335	
Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro	Leu	Thr	Ser	Leu	Thr	
			340					345						350		
Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu	Gly	Gly	Leu	Pro	Val	
	355						360					365				
Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	Leu	Ser	Gly	Val	Leu	Arg	
	370					375					380					
Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser	Pro	Ala	Ala	Gly	Asp	
385					390					395					400	
Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	
				405				410						415		
Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Gly	Pro	Gln	Val	
			420					425					430			
Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	
	435						440					445				
Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	
	450					455					460					
Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	
465					470					475					480	
Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	
				485				490						495		
Ala	Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	Pro	Ser	Ala	Ala	Ile	
			500					505					510			
Gly	Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	Ala	Met	Gly	Asn	Ser	
		515					520					525				
Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala	
						535					540					
Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu	
545					550					555					560	
Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp	
				565					570					575		

Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
580 585 590

Thr Ala Ala Ser
595

<210> 21
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB8.4 (DPV) cDNA

<400> 21
cgtggcaatg tcgttgaccg tcgggggccgg ggtcgccctcc gcagatcccg tggacgcggt 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgcccga cagttcaacg cctcaccggt ggcgcagtec tatttgccga atttcctcgc 180
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cggggggcggc 240
acagttacatc ggccctgtcg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgacccg gcatcgctcg cggggctagg ccagattgcc ccgctcctca 360
acggggccgca tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
caacggggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
gccgccaccg cggtaggagct 500

<210> 22
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB8.4 (DPV)

<400> 22
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

<210> 23
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>

<223> MTB9.8 (MSL)

<400> 23

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tggattccga tagcgggtttc ggcccctcga cgggcgacca cggcgcgag gcctccgaac 60
ggggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccggggcg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccctac 300
gggtcgaaag gagagatggt atgagccttt tggatgctca tatcccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cagcatcggg caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480
cccatgcccg gtttgtggcg gcggccgcc aagtcaacac cttgttgat gtcgcgcagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585
```

<210> 24

<211> 97

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> MTB9.8 (MSL)

<400> 24

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Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
  1                      5                      10                      15

Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
      20                      25                      30

Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
      35                      40                      45

Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
      50                      55                      60

Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
      65                      70                      75                      80

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
      85                      90                      95

Phe
```

<210> 25

<211> 1742

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> MTB9.9A (MTI, also known as MTI-A)

<220>

<221> modified_base

<222> (1)..(1742)

<223> n = g, a, c or t

<400> 25

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ccgctctctt tcaacgtcat aagttcgggtg ggccagtcgg ccgcgcgtgc atatggcacc 60
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aataacgcgt gtcccatgga taccgggacc gcacgacggt agagcggatc agcgcagccg 120
gtgccgaaca ctaccgcgtc cagctcagc cctgccgcgt tgcggaagat cgagcccagg 180
ttctcatggt cggttaacgc ttccaacact gcgacgggtgc gcgccccggc gaccacctga 240
gcaacgctcg gctccggcac ccggcgcgcg gctgccaaaca cccacgatt gagatggaag 300
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gg 1742

```

```

<210> 26
<211> 2836
<212> DNA
<213> Mycobacterium tuberculosis

```

```

<220>
<223> MTB9.9A (MTI also known as MTI-A)

```

```

<220>
<221> modified_base
<222> (104)
<223> n = g, a, c or t

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<400> 26
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cgattacccc caccgaaagg acgacgatcg ttcgtttgct cggtcagtcg tacttggcga 180
cgggcatggc gcggtttctt acctcgatcg cacagcagct gaccttcggc ccagggggca 240
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gccggcggt gtcggcgagt ttggcgcggg cggagccggg cgggagggtg tcggtgccgc 360
caagttgggc cgtcgcggct ccggccttcg cggagaagcc tgaggcgggc acgccgatgt 420
ccgtcatcgg cgaagcgtcc agctgcggtc agggaggcct gcttcgaggc ataccgctgg 480
cgagagcggg gcggcgatca ggcgccttcg ctcaccgata cgggttcgcg cacagcgtga 540
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cggcgggctg tgatgccaaa ttgaccgtcc cgacggggct ttatctgcgg caagatttca 720
tccccagccc ggtcgggtgg ccgataaata cgctgggtcag cgcgactctt ccggctgaat 780
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acgctgttac tgtggcggtt ccacagggtg atttgcggtg ccaactgggt aacacttgcg 900
aacgggtggc atcgaaatca acttgttgcg ttgcagtgat ctactctctt gcagagagcc 960

```

```

gttgctggga ttaattggga gaggaagaca gcatgtcggt cgtgaccaca cagccggaag 1020
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cggccgcggc tgctccaacc accggagtag tgcccgcagc cgccgatgaa gtatcagcgc 1140
tgaccgcggc tcagtttgct gcgcacgcgc agatgtacca aacgggtcagc gcccaggccg 1200
cggccattca cgaaatgttc gtgaacacgc tgggtggccag ttctgggtca tacgcggcca 1260
ccgaggcggc caacgcagcc gctgccggct gaacgggctc gcacgaacct gctgaaggag 1320
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tcggcgcca taacagcaga cgatctaggc attcagtact aaggagacag gcaacatggc 1440
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cgcccagacg gtggaggacg aggtctcgcc gatgtgggctg tccgcgcaaa acatttcggg 1560
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gagcatcagg ccatcgcttc tgatgtgttg gccgcgggtg acttttgggg cggcgccggt 1920
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aaccagccgc cgggttcgcg tgacatccct gacaatgagt tccgggtggg gttggcccgg 2520
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attcggcacg aggcacgagg cgggtgtcgg gacgacggga tcgatcacga tcatcgaccg 2760
gccgggatcc ttggcgatct cgttgagcac gaccggggcc cgcgggaagc tctgcgacat 2820
ccatgggttc ttcccg 2836

```

<210> 27

<211> 94

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> MTB9.9A (MTI, also known as MTI-A) ORF peptide

<400> 27

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
  1             5             10             15

```

```

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
      20             25             30

```

```

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
    35             40             45

```

```

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50             55             60

```

```

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
    65             70             75             80

```

```

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85             90

```

<210> 28
 <211> 1200
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB40 (HTCC#1) cDNA

<400> 28
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 tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
 ccgcggacaa atacgccggc aaaaaccgca accacgtgaa tttttccag gaactggcag 240
 acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcgggc cagacgaccc 300
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 cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
 tcatcacaaa cgcgctcaac ggctgaaag agctttggga caagctcacg ggggtgggtga 660
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 tgaccggcgc gaccagcggc ttgtcgaag tgaactggct gttcgggtgc gccggtctgt 780
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 agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
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<210> 29
 <211> 392
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB40 (HTCC#1)

<400> 29
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 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110

Arg	Pro	Val	Ala	Val	Asp	Leu	Thr	Tyr	Ile	Pro	Val	Val	Gly	His	Ala	
		115					120						125			
Leu	Ser	Ala	Ala	Phe	Gln	Ala	Pro	Phe	Cys	Ala	Gly	Ala	Met	Ala	Val	
	130					135					140					
Val	Gly	Gly	Ala	Leu	Ala	Tyr	Leu	Val	Val	Lys	Thr	Leu	Ile	Asn	Ala	
145					150					155					160	
Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	Leu	Ala	Glu	Leu	Val	Ala	Ala	
				165				170						175		
Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	Val	Ala	Asp	Ile	Ile	Lys	Gly	Thr	
			180					185					190			
Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys	
	195						200					205				
Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg	
	210					215					220					
Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr	
225					230					235					240	
Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala	
				245					250					255		
Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser	
			260					265					270			
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe	
		275					280						285			
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln	
	290					295						300				
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln	
305					310					315					320	
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met	
				325					330					335		
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser	
		340						345					350			
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr	
		355					360					365				
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln	
	370					375					380					
Lys	Val	Leu	Val	Arg	Asn	Val	Val									
385					390											

<210> 30

<211> 1441

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> MTB41 (MTCC#2) cDNA

<400> 30

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ttccggtccg gggccggagt cgatgctagc cgcccgggcc gcctgggacg gtgtggccgc 120
ggagttgact tccgcccggg tctcgtagtg atcgggtggtg tcgacgctga tcgttgagcc 180
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ccaggccgag tatgccgaaa tgtgggcccc agacgctgcc gtgatgtaca gctatgaggg 480
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cctggtgagc gtggctatcc gacgggcccgt tcacaccgct tgtagtagcg tacggctatg 1380
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g
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<210> 31

<211> 423

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> MTB41 (MTCC#2)

<400> 31

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Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
                20                      25                      30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
    35                      40                      45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
    50                      55                      60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
    65                      70                      75                      80

Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
                85                      90                      95

Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
    100                      105                      110
```

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

<210> 32
 <211> 154
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

<400> 32
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 aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
 gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 33
 <211> 51
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

<400> 33
 Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

<210> 34
 <211> 327
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Tb38-1 or 38-1 (MTb11)

<400> 34
 cggcacgaga gaccgatgcc gctaccctcg cgcaggaggc aggtaatttc gagcggatct 60
 ccggcgacct gaaaaccagc atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120
 agtggcgcgg cgcggcgggg acggccgccc aggcgcgggt ggtgcgcttc caagaagcag 180
 ccaataagca gaagcaggaa ctcgacgaga tctcgacgaa tattcgtcag gccggcgctc 240
 aatactcgag ggccgacgag gagcagcagc aggcgcgtgtc ctcgcaaattg ggcttctgac 300
 ccgctaatac gaaaagaaac ggagcaa 327

<210> 35
 <211> 95
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Tb38-1 or 38-1 (MTb11)

<400> 35
 Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

<210> 36
 <211> 542
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa3

<220>
 <221> modified_base
 <222> (406)
 <223> n = g, a, c or t

<400> 36
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 cattgagcag gacatggccg tggacagcgc cggcaagatc acctaccgca tcaagctcga 180
 agtgtcgttc aagatgaggc cggcgcaacc gcgctagcac gggccggcga gcaagacgca 240
 aaatcgacag gtttgcggtt gattcgtgcg attttgtgtc tgctcgccga ggcctaccag 300
 gcgcggccca ggtccgcgtg ctgccgtatc caggcgtgca tcgcgattcc ggcggccacg 360
 ccggagttaa tgcttcgcgt cgaccgaac tgggcgatcc gccggngagc tgatcgatga 420
 ccgtggccag cccgtcgatg cccgagttgc ccgaggaaac gtgctgccag gccggtagga 480
 agcgtccgta ggcggcggtg ctgaccggct ctgcctgcgc cctcagtgcg gccagcgagc 540
 gg 542

<210> 37
 <211> 66
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa3

<400> 37
 Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1 5 10 15
 Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20 25 30

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45

Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60

Pro Arg
 65

<210> 38
 <211> 1993
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 38 kD

<400> 38
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 agcatgcgga aaccgcccga tacgtcgccg gactgtcggg ggacgtcaag gacgccaagc 120
 gcggaaattg aagagcacag aaaggatatg cgtgaaaatt cgtttgcata cgctgttggc 180
 cgtgttgacc gctgcgccgc tgctgctagc agcggcgggc tgtggctcga aaccaccgag 240
 cggttcgctt gaaacgggag ccggcgccgc tactgtcgcg actacccccg cgtcgtcgcc 300
 ggtgacgttg gcggagaccg gtagcacgct gctctaccgc ctgttcaacc tgtgggggtcc 360
 ggcctttcac gagaggtatc cgaacgtcac gatcaccgct cagggcaccg gttctggtgc 420
 cgggatcgcg caggccgccc ccgggacggt caacattggg gcctccgacg cctatctgtc 480
 ggaagggtgat atggccgccc acaaggggct gatgaacatc gcgctagcca tctccgctca 540
 gcagggtcaac tacaacctgc ccggagttag cgagcacctc aagctgaacg gaaaagtcct 600
 ggccggccatg taccagggca ccatcaaaac ctgggacgac ccgcagatcg ctgcgtcaa 660
 ccccgccgctg aacctgcccg gcaccgcggt agttccgctg caccgctccg acgggtcccg 720
 tgacaccttc ttgttcaccc agtacctgtc caagcaagat cccgagggct ggggcaagtc 780
 gcccggtctt gccaccaccg tcgacttccc ggccggtgccc ggtgcgctgg gtgagaacgg 840
 caacggcgcc atggtgaccg gttgcgccga gacaccgggc tgcgtggcct atatcgccat 900
 cagcttcttc gaccaggcca gtcaacgggg actcggcgag gcccaactag gcaatagctc 960
 tggcaatttc ttgttgcccg acgcgcaaag cattcaggcc gcggcggtcg gcttcgcatc 1020
 gaaaaccccc gcgaaccagg cgatttcgat gatcgacggg cccgcccccg acggctaccc 1080
 gatcatcaac tacgagtacg ccatcgtaa caaccggcaa aaggacgccg ccaccgcgca 1140
 gaccttgacg gcatttctgc actgggcgat caccgacggc aacaaggcct cgttcctcga 1200
 ccagggttat ttccagccgc tgccgcccgc ggtggtgaa ttgtctgacg cgttgatcgc 1260
 gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgct gggccatcgg 1320
 gctgcttttc ggagcatgct ggcccgtgcc ggtgaagtcg gccgcgctgg cccggccatc 1380
 cgggtggttg gtgggtagg tgccgtgatc ccgctgcttg cgtggtctt ggtgctggtg 1440
 gtgctggtca tcgaggcgat ggggtgcgat aggtcacaac ggttgcatct cttaccgccc 1500
 accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccac 1560
 cggtcggcgc ctactacggg gcgttgcccg tgatcgctcg gacgtggcg acctcgcaa 1620
 tcgccctgat catcgcggtg ccggtctctg taggagcggc gctggtgatc gtggaacggc 1680
 tgccgaaacg gttggccgag gctgtgggaa tagtcttgga attgctcgcc ggaatcccca 1740
 gcgtggtcgt cggtttgtgg ggggcaatga cgttcgggac gttcatcgct catcacatcg 1800
 ctccggtgat cgctcacaac gctcccgatg tgccggtgct gaactacttg cgcggcgacc 1860
 cgggcaacgg ggagggcatg ttggtgtccg gtctggtggt ggccggtgat gtcgttccca 1920
 ttatcgccac caccactcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
 cgatcgggaa ttc 1993

<210> 39
 <211> 374
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>

<223> 38 kD

<400> 39

Met	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro
1				5					10					15	
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser
			20					25					30		
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
			35				40					45			
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu
	50					55					60				
Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr
65					70					75					80
Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	Ala
			85						90					95	
Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly
			100					105					110		
Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser
	115						120					125			
Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys
	130					135					140				
Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr
145					150					155					160
Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	Leu	Pro
				165					170					175	
Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly	Asp	Thr
			180					185					190		
Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly	Trp	Gly
	195						200					205			
Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val	Pro	Gly
	210					215					220				
Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu
225				230						235					240
Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp	Gln	Ala
				245					250					255	
Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser	Gly	Asn
			260					265					270		
Phe	Leu	Leu	Pro	Asp	Ala	Gln	Ser	Ile	Gln	Ala	Ala	Ala	Ala	Gly	Phe
	275						280					285			
Ala	Ser	Lys	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Ser	Met	Ile	Asp	Gly	Pro
	290					295					300				

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
305 310 315 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
325 330 335

His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
340 345 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
355 360 365

Ile Ala Thr Ile Ser Ser
370

<210> 40
<211> 999
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 40
atgcatcacc atcaccatca catgcatcag gtggacccca acttgacacg tcgcaagggga 60
cgattggcgg cactggctat cgcggcgatg gccagcgcca gcctgggtgac cgttgcggtg 120
cccgcgaccg ccaacgccga tccggagcca gcgcccccg taccacaac ggccgcctcg 180
ccgccgtcga ccgctgcagc gccaccgcga ccggcgacac ctggtgcccc cccaccaccg 240
gccgccgcca acacgccgaa tgcccagccg ggcgatccca acgcagcacc tccgcgggcc 300
gaccggaacg caccgccggc acctgtcatt gccccaaacg caccccaacc tgtccggatc 360
gacaaccggg ttggaggatt cagcttcgcg ctgcctgctg gctgggtgga gtctgacgcc 420
gccacttcg actacggttc agcactctc agcaaaacca ccggggaccc gccatttccc 480
ggacagccgc cgccggtggc caatgacacc cgtatcgtgc tcggccggct agacaaaag 540
ctttacgcca gcgccgaagc caccgactcc aaggccgcgg ccggttggg ctcggacatg 600
ggtgagttct atatgcccta cccgggcacc cggatcaacc aggaaaccgt ctcgctcgac 660
gccaacgggg tgtctggaag cgctcgtat tacgaagtca agttcagcga tccgagtaag 720
ccgaacggcc agatctggac gggcgtaate ggctcgcccc cggcgaacgc accggacgcc 780
gggccccctc agcgctgggt tgtggtatgg ctccgggaccg ccaacaaccc ggtggacaag 840
ggcgccgcca aggcgctggc cgaatcgatc cggcctttgg tcgccccgcc gccggcgccg 900
gcaccggctc ctgcagagcc cgctccggcg ccggcgccgg ccggggaagt cgctcctacc 960
ccgacgacac cgacaccgca gcggacctta ccggcctga 999

<210> 41
<211> 332
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 41
Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45

Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr	50	55	60
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro	65	70	75
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala	85	90	95
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro	100	105	110
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser	115	120	125
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp	130	135	140
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro	145	150	155
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg	165	170	175
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala	180	185	190
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro	195	200	205
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val	210	215	220
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys	225	230	235
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn	245	250	255
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly	260	265	270
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu	275	280	285
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro	290	295	300
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr	305	310	315
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala					325	330	

<210> 42

<211> 702

<212> DNA

<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

<400> 42
cggcacgagg atcggtagccc cgcggcatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcatacaat tagtgcagga acctttcagt ttagcgacga taatggctat 180
agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacgggtg gatcagcaag 240
agatTTTTgaa cagggccaac gaggtggagg ccccgatggc ggacccaccg actgatgtcc 300
ccatcacacc gtgcgaactc acgngggnta aaaacgccgc ccaacagntg gtnttgtccg 360
ccgacaacat gcgggaatac ctggcggccg gtgcaaaga gcggcagcgt ctggcgacct 420
cgctgcgcaa cgcggccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaact gtgcaggcag aatcggccgg gcccgtcgga ggggacagtt 540
cggccgaact aaccgatacg ccgaggggtg ccacggccgg tgaacccaac ttcatggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcacgcctc gcgcactgng 660
gggatgggtg gaacacttnc acctgacgc tgcaaggcga cg 702

<210> 43
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

<400> 43
Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15
Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30
His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45
Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60
Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80
Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95
Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100 105 110
Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115 120 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
130 135 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145 150 155 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165 170 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180 185 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195 200 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
275 280 285

<210> 44
<211> 339
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPPD genomic DNA

<400> 44
atgaagttga agtttgctcg cctgagtact gcgatactgg gttgtgcagc ggcgcttgtg 60
tttcctgcct cggttgccag cgcagatcca cctgaccgc atcagccgga catgacgaaa 120
ggctattgcc cgggtggccg atggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180
taccgccgacg gtcggttttg gcaccagtgg atgcaaactt gggtttaccgg cccacagttt 240
tacttcgatt gtgtcagcgg cggtgagccc ctccccggcc cgccgccacc ggggtggttc 300
gggtggggcaa ttccgtccga gcagcccaac gctccctga 339

<210> 45
<211> 112
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 45
Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15

Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30

Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45

Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60

Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80

Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95

Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100 105 110

<210> 46

<211> 921

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:tri-fusion
protein DPV-MTI-MSL (designated MTb31F) cDNA

<220>

<221> CDS

<222> (1)..(900)

<223> MTb31F

<400> 46

cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Leu Asn Ala Thr Asp
20 25 30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
35 40 45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
50 55 60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
65 70 75 80

gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
85 90 95

tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag 336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
100 105 110

gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg	384
Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu	
115 120 125	
gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag	432
Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu	
130 135 140	
ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc	480
Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala	
145 150 155 160	
aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa	528
Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln	
165 170 175	
acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg	576
Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
180 185 190	
gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc	624
Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala	
195 200 205	
aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg	672
Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala	
210 215 220	
atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag	720
Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln	
225 230 235 240	
gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg	768
Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu	
245 250 255	
ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg	816
Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
260 265 270	
gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc cat	864
Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His	
275 280 285	
cac act ggc ggc cgc tcg agc aga tcc ggc tgc taa caaagcccga	910
His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys	
290 295 300	
aaggaagctg a	921

<210> 47

<211> 299

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: tri-fusion
protein DPV-MTI-MSL (designated MTb31F) cDNA

<400> 47

His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp	20	25	30
Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr	35	40	45
Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	50	55	60
Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val	65	70	75
Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Leu	Met	Thr	Ile	Asn	85	90	95
Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	100	105	110
Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	115	120	125
Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	130	135	140
Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	145	150	155
Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	165	170	175
Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu	180	185	190
Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	195	200	205
Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	210	215	220
Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	225	230	235
Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	245	250	255
Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	260	265	270
Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	Phe	Asp	Ile	His	275	280	285
His	Thr	Gly	Gly	Arg	Ser	Ser	Arg	Ser	Gly	Cys						290	295	

<210> 48

<211> 2168

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:tetra-fusion
 protein DPV-MTI-MSL-MTCC#2 (designated MTb71F)

<220>
 <221> CDS
 <222> (1)..(2133)
 <223> MTb71F

<400> 48
 cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
 His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 5 10 15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
 Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 50 55 60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65 70 75 80

gag tgc gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
 Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 85 90 95

tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag 336
 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110

gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg 384
 Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
 115 120 125

gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag 432
 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140

ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc 480
 Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160

aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa 528
 Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
 165 170 175

acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg 576
 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
 180 185 190

gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc 624
 Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 195 200 205

aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala 210 215 220	672
atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln 225 230 235 240	720
gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu 245 250 255	768
ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val 260 265 270	816
gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc atg Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met 275 280 285	864
gat ttc ggg ctt tta cct ccg gaa gtg aat tca agc cga atg tat tcc Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser 290 295 300	912
ggt ccg ggg ccg gag tcg atg cta gcc gcc gcg gcc gcc tgg gac ggt Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly 305 310 315 320	960
gtg gcc gcg gag ttg act tcc gcc gcg gtc tcg tat gga tcg gtg gtg Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val 325 330 335	1008
tcg acg ctg atc gtt gag ccg tgg atg ggg ccg gcg gcg gcc gcg atg Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met 340 345 350	1056
gcg gcc gcg gca acg ccg tat gtg ggg tgg ctg gcc gcc acg gcg gcg Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala 355 360 365	1104
ctg gcg aag gag acg gcc aca cag gcg agg gca gcg gcg gaa gcg ttt Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe 370 375 380	1152
ggg acg gcg ttc gcg atg acg gtg cca cca tcc ctc gtc gcg gcc aac Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn 385 390 395 400	1200
cgc agc cgg ttg atg tcg ctg gtc gcg gcg aac att ctg ggg caa aac Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn 405 410 415	1248
agt gcg gcg atc gcg gct acc cag gcc gag tat gcc gaa atg tgg gcc Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala 420 425 430	1296
caa gac gct gcc gtg atg tac agc tat gag ggg gca tct gcg gcc gcg Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala 435 440 445	1344

tcg gcg ttg ccg ccg ttc act cca ccc gtg caa ggc acc ggc ccg gcc	1392
Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala	
450 455 460	
ggg ccc gcg gcc gca gcc gcg gcg acc caa gcc gcc ggt gcg ggc gcc	1440
Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala	
465 470 475 480	
gtt gcg gat gca cag gcg aca ctg gcc cag ctg ccc ccg ggg atc ctg	1488
Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu	
485 490 495	
agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg aca tcg	1536
Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser	
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gga ctg ttg ggg atc gcg tcg acc ctc aac ccg caa gtc gga tcc gct	1584
Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala	
515 520 525	
cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg	1632
Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala	
530 535 540	
ctc tac att gca tcc atc gcg acc ggc agc att gcg ctc gcg atc acg	1680
Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr	
545 550 555 560	
aac acg gcc aga ccc tgg cac atc ggc cta tac ggg aac gcc ggc ggg	1728
Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly	
565 570 575	
ctg gga ccg acg cag ggc cat cca ctg agt tcg gcg acc gac gag ccg	1776
Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro	
580 585 590	
gag ccg cac tgg ggc ccc ttc ggg ggc gcg gcg ccg gtg tcc gcg ggc	1824
Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly	
595 600 605	
gtc ggc cac gca gca tta gtc gga gcg ttg tcg gtg ccg cac agc tgg	1872
Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp	
610 615 620	
acc acg gcc gcc ccg gag atc cag ctc gcc gtt cag gca aca ccc acc	1920
Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr	
625 630 635 640	
ttc agc tcc agc gcc ggc gcc gac ccg acg gcc cta aac ggg atg ccg	1968
Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro	
645 650 655	
gca ggc ctg ctc agc ggg atg gct ttg gcg agc ctg gcc gca cgc ggc	2016
Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly	
660 665 670	
acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa	2064
Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln	
675 680 685	

gag gac ggc cgc aaa ccc ccg gta gtt gtg att aga gag cag ccg ccg 2112
 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
 690 695 700

ccc gga aac ccc ccg cgg taa gattttctaaa tccatcacac tggcggccgc 2163
 Pro Gly Asn Pro Pro Arg
 705 710

tcgag 2168

<210> 49
 <211> 710
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tetra-fusion
 protein DPV-MTI-MSL-MTCC#2 (designated MTb71F)

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 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30
 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45
 Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 50 55 60
 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65 70 75 80
 Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 85 90 95
 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110
 Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
 115 120 125
 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140
 Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160
 Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
 165 170 175
 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
 180 185 190
 Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 195 200 205
 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
 210 215 220

Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	225	230	235	240
Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	245	250		255
Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	260	265		270
Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	Phe	Asp	Ile	Met	275	280		285
Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr	Ser	290	295	300	
Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp	Gly	305	310	315	320
Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val	Val	325	330		335
Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala	Met	340	345		350
Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala	Ala	355	360		365
Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala	Phe	370	375	380	
Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala	Asn	385	390	395	400
Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln	Asn	405	410		415
Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp	Ala	420	425		430
Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala	Ala	435	440		445
Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro	Ala	450	455	460	
Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly	Ala	465	470	475	480
Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile	Leu	485	490		495
Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr	Ser	500	505		510
Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser	Ala	515	520		525
Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile	Ala	530	535	540	

Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
 545 550 555 560
 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
 565 570 575
 Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
 580 585 590
 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
 595 600 605
 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
 610 615 620
 Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
 625 630 635 640
 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655
 Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
 660 665 670
 Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
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 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
 690 695 700
 Pro Gly Asn Pro Pro Arg
 705 710

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 <213> Mycobacterium tuberculosis

<220>
 <223> Ra35 N-terminus of MTB32A (Ra35FL)

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 aacaacgccg tgggcgcggg gaccggcatc gtcatcgatc ccaacgggtg cgtgctgacc 180
 aacaaccacg tgatcgcggg cgccaccgac atcaatgctg tcagegctcg ctccggccaa 240
 acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgcggt gctgcagctg 300
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 gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480
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 gtcaacggcc taggacaggt ggtcgggtatg aacacggccg cgtcctag 588